



#8

PATENT
Docket No. 511582002410

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Tami M. Procopio
Tami M. Procopio

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Arthur B. RAITANO, *et al.*

Serial No.: 10/017,066

Filing Date: 14 December 2001

For: NOVEL G PROTEIN-COUPLED
RECEPTOR UP-REGULATED IN
PROSTATE CANCER AND USES
THEREOF

Examiner: To Be Assigned

Group Art Unit: 1642

SUBMISSION OF SUBSTITUTE DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

Attached please find 27 sheet(s) of substitute drawings in connection with the above-identified application.

Respectfully submitted,

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Registration No. 29,959

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FIG. 1A

9	18	27	36	45	54
5' CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG					

63	72	81	90	99	108
ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC					

117	126	135	144	153	162
TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT					

M	M	V	D	P	N
171	180	189	198	207	216
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

A	T	Y	F	I	L
225	234	243	252	261	270
TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA					

L	A	F	P	L	C
279	288	297	306	315	324
ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT					

I	I	Y	I	V	R
333	342	351	360	369	378
CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA					

L	C	M	L	S	G
387	396	405	414	423	432
ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG					

M	L	A	I	F	W
441	450	459	468	477	486
CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG					

L	Q	I	F	A	I
495	504	513	522	531	540
GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA					

A	M	A	F	D	R
549	558	567	576	585	594
GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG					

V	L	T	L	P	R
603	612	621	630	639	648
GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC					

A	A	L	M	A	P
63	72	81	90	99	108
ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC					

P	V	F	I	K	Q
64	73	82	91	100	109
GTC TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT					

L	N	G	N	E	S
65	74	83	92	101	110
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
66	75	84	93	102	111
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
67	76	85	94	103	112
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
68	77	86	95	104	113
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
69	78	87	96	105	114
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
70	79	88	97	106	115
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
71	80	89	98	107	116
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
72	81	90	109	118	127
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
73	82	91	110	129	138
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
74	83	92	111	130	139
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
75	84	93	112	131	140
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
76	85	94	113	132	141
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
77	86	95	114	133	142
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
78	87	96	115	134	143
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
79	88	97	116	135	144
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
80	89	98	117	136	145
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
81	90	99	118	137	146
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
82	91	100	119	138	147
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
83	92	101	120	139	148
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
84	93	102	121	140	149
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
85	94	103	122	141	150
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
86	95	104	123	142	151
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
87	96	105	124	143	152
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
88	97	106	125	144	153
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
89	98	107	126	145	154
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
90	99	108	127	146	155
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
91	100	109	128	147	156
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
92	101	110	129	148	157
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
93	102	111	130	149	158
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
94	103	112	131	150	159
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
95	104	113	132	151	160
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
96	105	114	133	152	161
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

S	S	S	S	S	S
97	106	115	134	153	162
GCT ACA TAC TTC ATC CTA ATA CGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG					

FIG. 1B

657	666	675	684	693	702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC					
S N I L S H S Y C L H Q D V M K L A					
711	720	729	738	747	756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC					
C D D I R V N V V Y G L I V I I S A					
765	774	783	792	801	810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT					
I G L D S L L I S F S Y L L I L K T					
819	828	837	846	855	864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT					
V L G L T R E A Q A K A F G T C V S					
873	882	891	900	909	918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG					
H V C A V F I F Y V P F I G L S M V					
927	936	945	954	963	972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC					
H R F S K R R D S P L P V I L A N I					
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG					
Y L L V P P V L N P I V Y G V K T K					
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG					
E I R Q R I L R L F H V A T H A S E					
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT					
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA					
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT					
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC					
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA					

FIG. 1C

1359	1368	1377	1386	1395	1404
AAC TGC TTC TAC TGA TGG TTT ACA GCA TTC TGA GAT AAG AAT GGT ACA TCT AGA					
-----	-----	-----	-----	-----	-----
1413	1422	1431	1440	1449	1458
GAA CAT TTG CCA AAG GCC TAA GCA CGG CAA AGG AAA ATA AAC ACA GAA TAT AAT					
-----	-----	-----	-----	-----	-----
1467	1476	1485	1494	1503	1512
AAA ATG AGA TAA TCT AGC TTA AAA CTA TAA CTT CCT CTT CAG AAC TCC CAA CCA					
-----	-----	-----	-----	-----	-----
1521	1530	1539	1548	1557	1566
CAT TGG ATC TCA GAA AAA TGC TGT CTT CAA AAT GAC TTC TAC AGA GAA GAA ATA					
-----	-----	-----	-----	-----	-----
1575	1584	1593	1602	1611	1620
ATT TTT CCT CTG GAC ACT AGC ACT TAA GGG GAA GAT TGG AAG TAA AGC CTT GAA					
-----	-----	-----	-----	-----	-----
1629	1638	1647	1656	1665	1674
AAG AGT ACA TTT ACC TAC GTT AAT GAA AGT TGA CAC ACT GTT CTG AGA GTT TTC					
-----	-----	-----	-----	-----	-----
1683	1692	1701	1710	1719	1728
ACA GCA TAT GGA CCC TGT TTT TCC TAT TTA ATT TTC TTA TCA ACC CTT TAA TTA					
-----	-----	-----	-----	-----	-----
1737	1746	1755	1764	1773	1782
GGC AAA GAT ATT ATT AGT ACC CTC ATT GTA GCC ATG GGA AAA TTG ATG TTC AGT					
-----	-----	-----	-----	-----	-----
1791	1800	1809	1818	1827	1836
GGG GAT CAG TGA ATT AAA TGG GGT CAT ACA AGT ATA AAA ATT AAA AAA AAA AAA					
-----	-----	-----	-----	-----	-----
1845	1854	1863	1872	1881	1890
GAC TTC ATG CCC AAT CTC ATA TGA TGT GGA AGA ACT GTT AGA GAG ACC AAC AGG					
-----	-----	-----	-----	-----	-----
1899	1908	1917	1926	1935	1944
GTA GTG GGT TAG AGA TTT CCA GAG TCT TAC ATT TTC TAG AGG AGG TAT TTA ATT					
-----	-----	-----	-----	-----	-----
1953	1962	1971	1980	1989	1998
TCT TCT CAC TCA TCC AGT GTT GTA TTT AGG AAT TTC CTG GCA ACA GAA CTC ATG					
-----	-----	-----	-----	-----	-----
2007	2016	2025	2034	2043	2052
GCT TTA ATC CCA CTA GCT ATT GCT TAT TGT CCT GGT CCA ATT GCC AAT TAC CTG					
-----	-----	-----	-----	-----	-----
2061	2070	2079	2088	2097	2106
TGT CTT GGA AGA AGT GAT TTC TAG GTT CAC CAT TAT GGA AGA TTC TTA TTC AGA					
-----	-----	-----	-----	-----	-----
2115	2124	2133	2142	2151	2160
AAG TCT GCA TAG GGC TTA TAG CAA GTT ATT TAT TTT TAA AAG TTC CAT AGG TGA					
-----	-----	-----	-----	-----	-----
2169	2178	2187	2196	2205	2214
TTC TGA TAG GCA GTG AGG TTA GGG AGC CAC CAG TTA TGA TGG GAA GTA TGG AAT					
-----	-----	-----	-----	-----	-----
2223	2232	2241	2250	2259	2268
GGC AGG TCT TGA AGA TAA CAT TGG CCT TTT GAG TGT GAC TCG TAG CTG GAA AGT					
-----	-----	-----	-----	-----	-----
2277	2286	2295	2304	2313	2322
GAG GGA ATC TTC AGG ACC ATG CTT TAT TTG GGG CTT TGT GCA GTA TGG AAC AGG					
-----	-----	-----	-----	-----	-----
2331	2340	2349	2358	2367	2376
GAC TTT GAG ACC AGG AAA GCA ATC TGA CTT AGG CAT GGG AAT CAG GCA TTT TTG					
-----	-----	-----	-----	-----	-----

FIG. 1D

FIG. 2

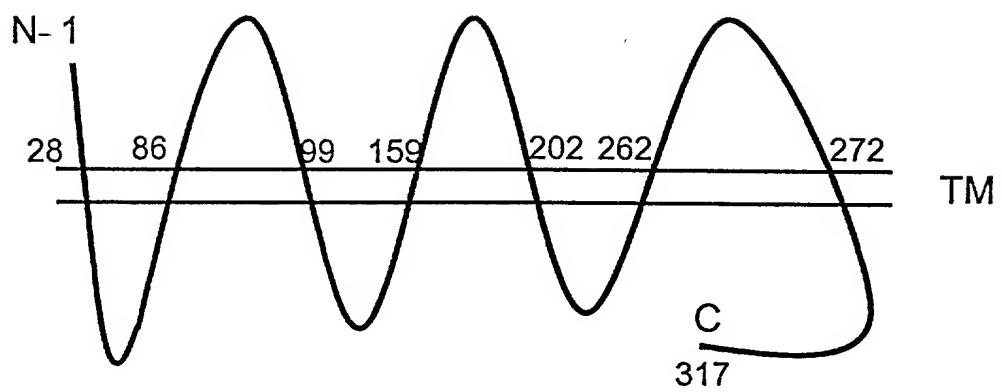
1	101P3A11	15 16	30 31	45 46	60 61	75 76	90
2	RA1C	-MSSCN--	FTHATF	MJIGIPGLEEAHFWP	GFPILLSMYAVALFGN	CIVVFLVRTERSLHA	PMTFLCMIAAIDLA
3	HPRAJ70	-MSSCN--	FTHATC	VLIGIPGLEKAHFHW	GFPILLSMYAVAMCGN	CIVVFLVRTERSLHA	PMTFLCMIAAIDLA
91		105 106	120 121	135 136	150 151	165 166	180
1	101P3A11	NSTTIQFDACLLQIF	AIHSLSGMESTILLA	MAFDRYVAICHPLRH	AFTVLTLPRTVKIGVA	AVVRGAALMAPLPVF	IKQIUPFCRSNLISHS
2	RA1C	DSREITFDACLAQMF	FIHALSAESTILLA	MAFDRYVAICHPLRH	AAYVNNTTVTQIGMV	AIVRGSLFFFPLPLL	IKR1AFCHSNVLISHS
3	HPRAJ70	DSREISIEACTQMF	FIHALSAESTILLA	MAFDRYVAICHPLRH	AAYVNNTTVTQIGIV	AVVRGSLFFFPLPLL	IKR1AFCHSNVLISHS
181		195 196	210 211	225 226	240 241	255 256	270
1	101P3A11	YCLHQDVMKIAACDDI	RVNVVYGLIVLISAI	GLDSLISFSYLLIL	KTVGLIT-REAQAKA	FGTCVSHVCNAVFFFY	VBFIGLSMVHRFNSKR
2	RA1C	YCVHQDVMKLAYDT	LPNVVYGLTAILLM	GVDVMEISLSYFLII	RAVLQLPSKSERAKA	FGTCVSHIGVVLAFY	VPLIGLSVVHRFNS
3	HPRAJ70	YCVHQDVMKLAYDT	LPNVVYGLTAILLM	GVDVMEISLSYFLII	RTVLQLPSKSERAKA	FGTCVSHIGVVLAFY	VPLIGLSVVHRFNS
271		285 286	300 301	315 316	330 331	345 346	360
1	101P3A11	RDSPLPVTLANTYLL	YPPVLNPTVYGVTK	EIRORLRLFHVATH	A5EP-----		
2	RA1C	LDPVIVHVMGDVYLL	LPPVINPLIYGAKTK	QIRTRVLMFKISCD	KDIENGGNT		
3	HPRAJ70	LHPTIVRVVNGDVIYLL	LPPVINPLIYGAKTK	QIRTRVLMFKISCD	KDLQAVGGK		

FIG. 3

GATCAAACCTTTCCATTCAAGAGTCCTCTGATTCAAGATTTAACATTGGAAAGACAGTATTCAGAAAAAA
AATTCCCTTAATAAAAATACAACTCAGATCCTCAAATATGAAACTGGTTGGGAATCTCCATTTCATATTATT
TCTCTTGTTTCTTGCTACGTATAATTATTAATATCCTGACTAGGTTGGGGTTATTACTTTCATTTA
CCATGCAGTCAAATCTAAACTGCTTCACTGATGGTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATT
TGCAAAGGCCAAGCACAGCAAAGGAAAATAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACT
TCCTCTTAGAACTCCCAACCACATTGGATC

FIG. 4

Extracellular



Intracellular

FIG. 5A

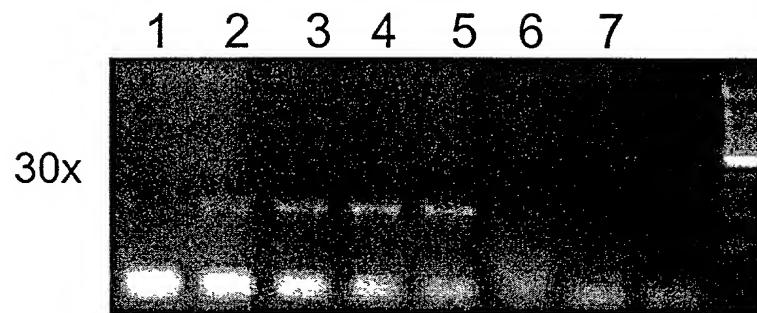


FIG. 5B

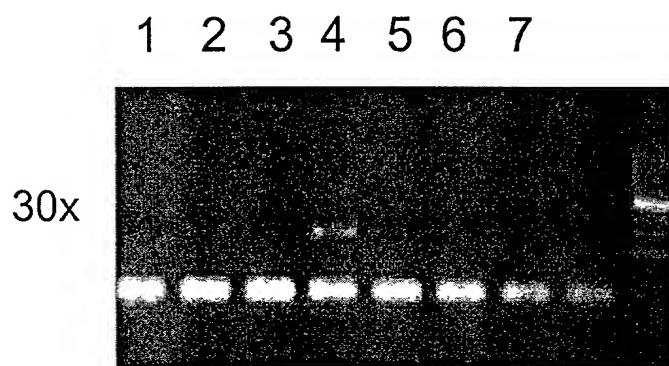


FIG. 6A

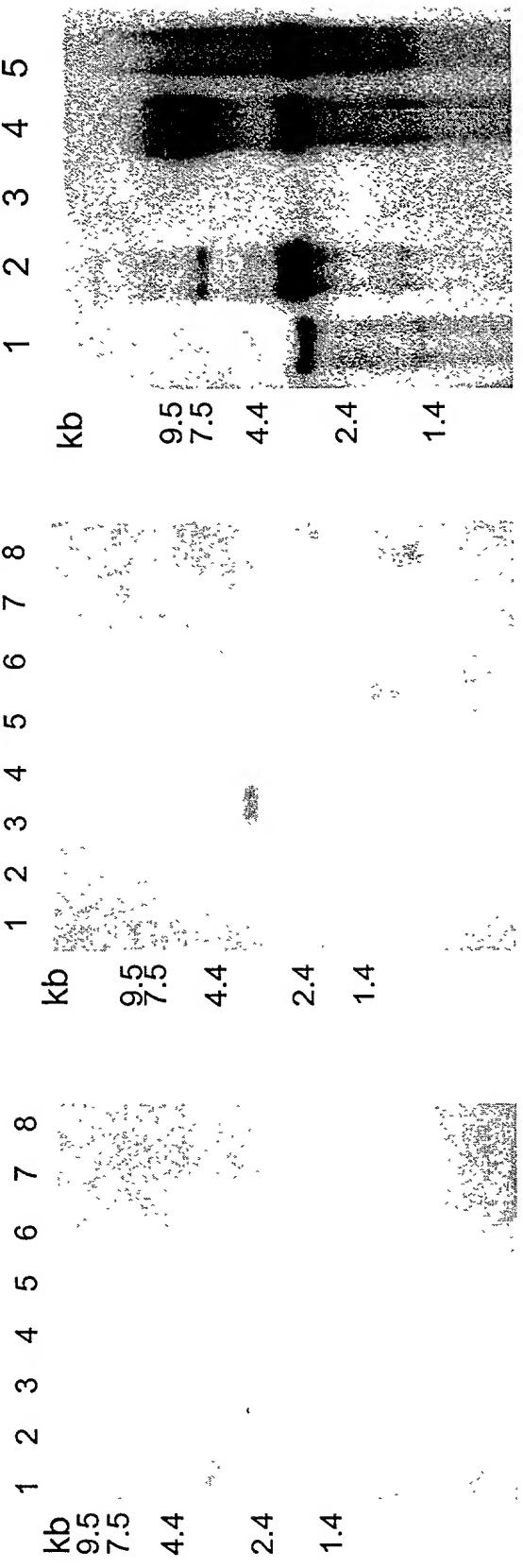


FIG. 6B

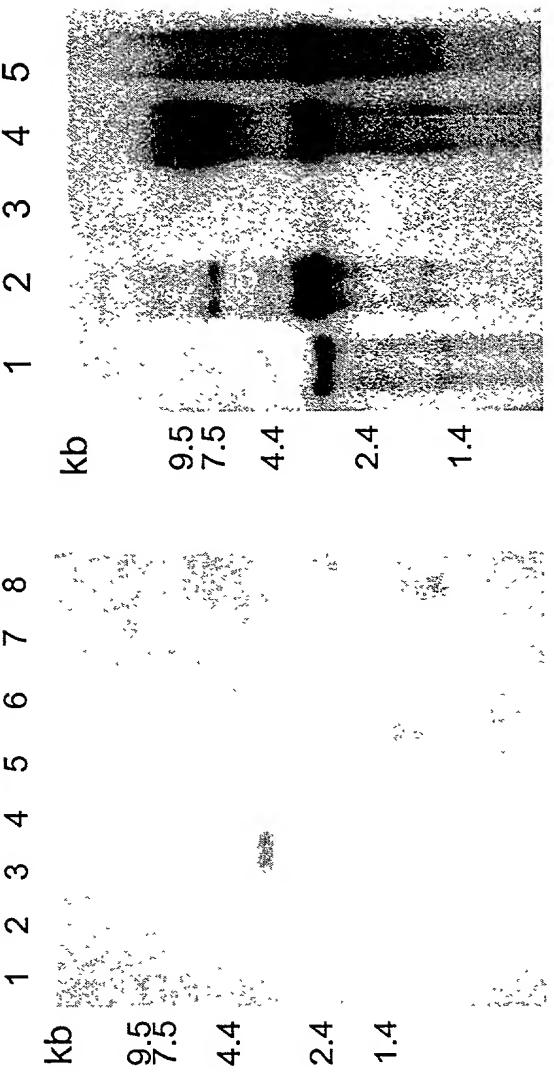


FIG. 6C

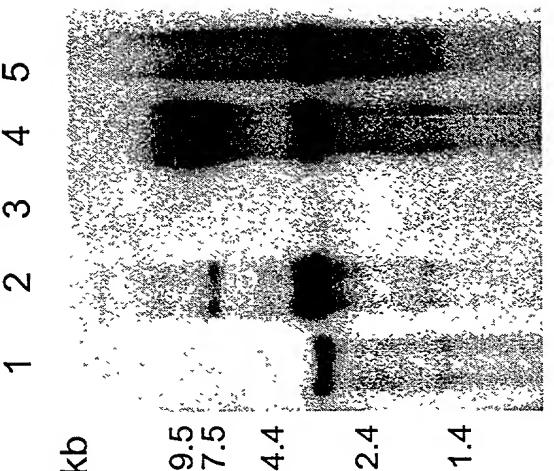


FIG. 7

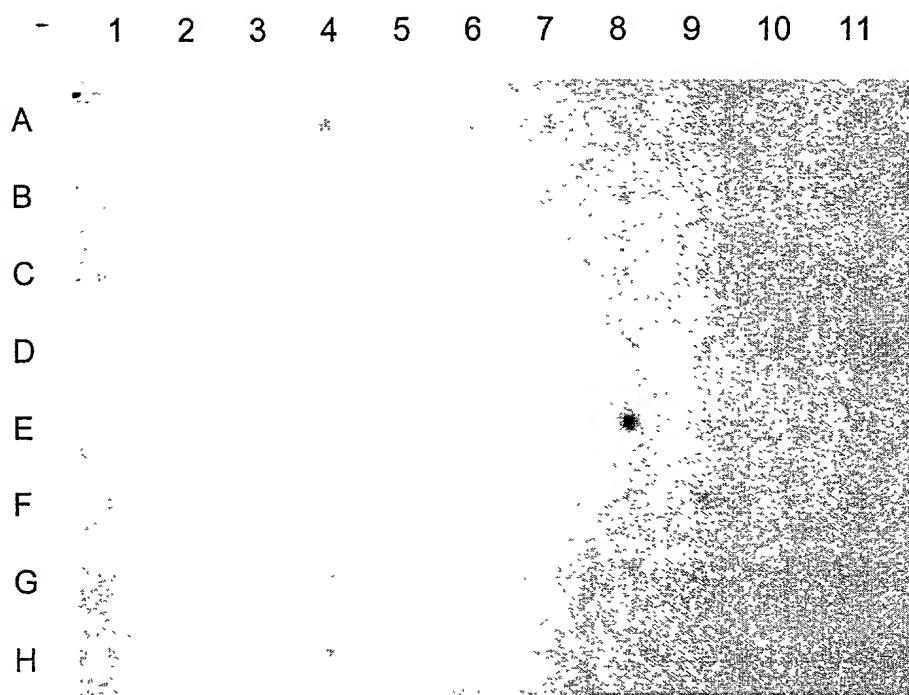


FIG. 8A

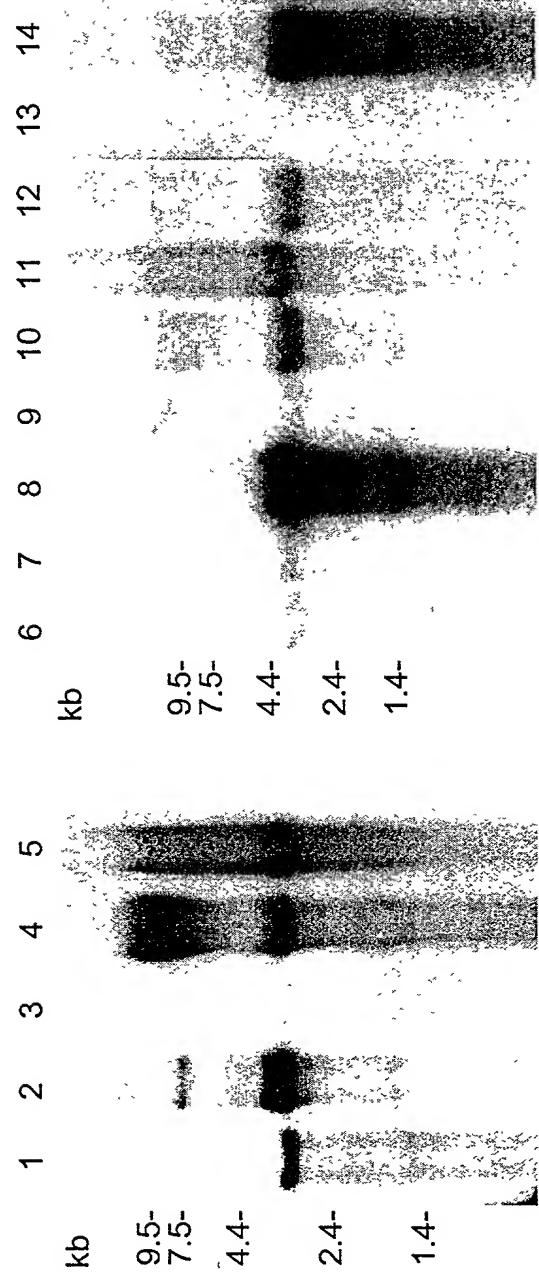


FIG. 8B

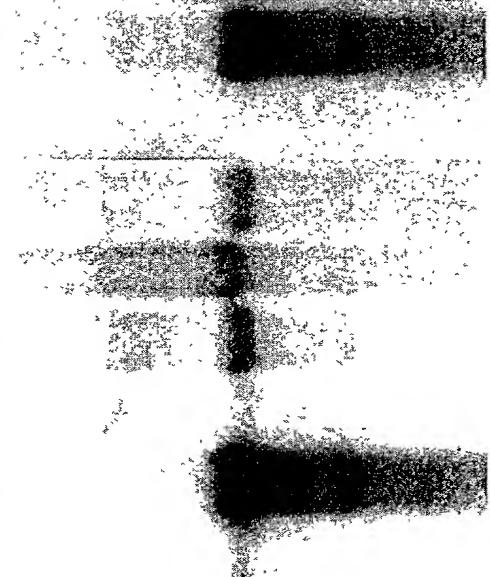


Figure 9A

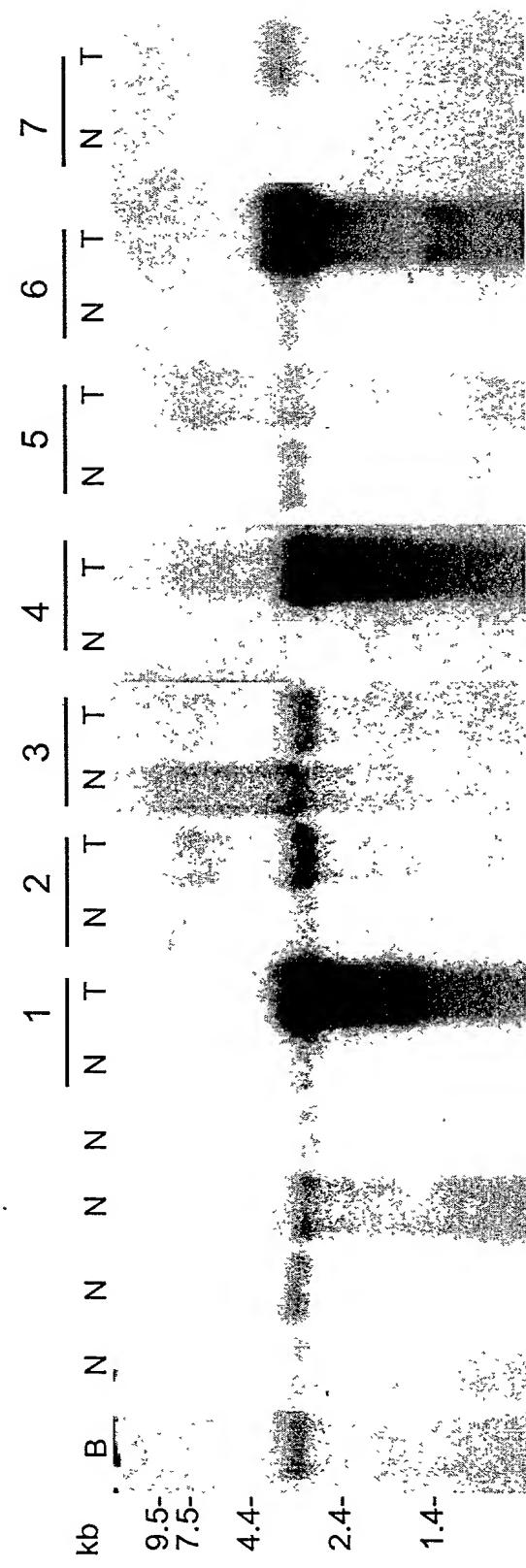


Figure 9B

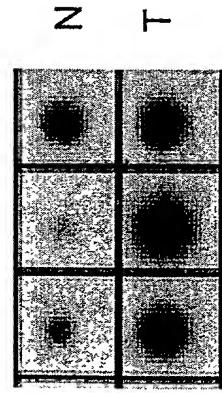


Figure 10

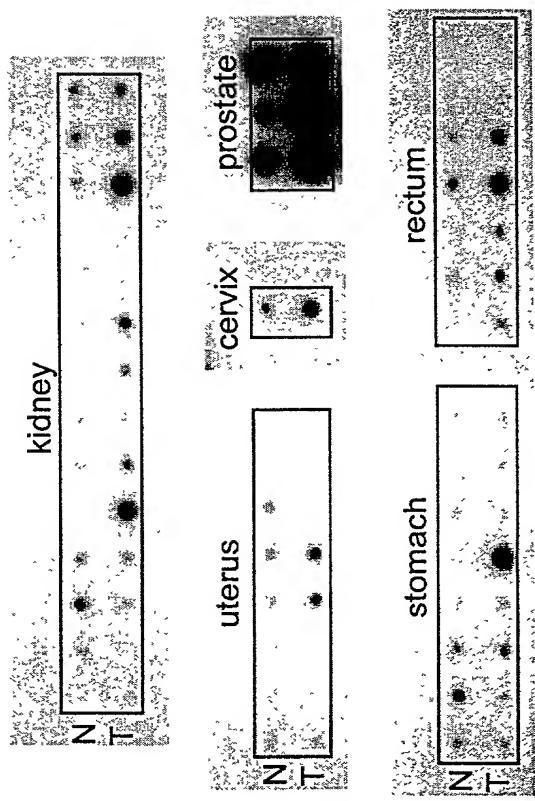


Figure 11A-11B

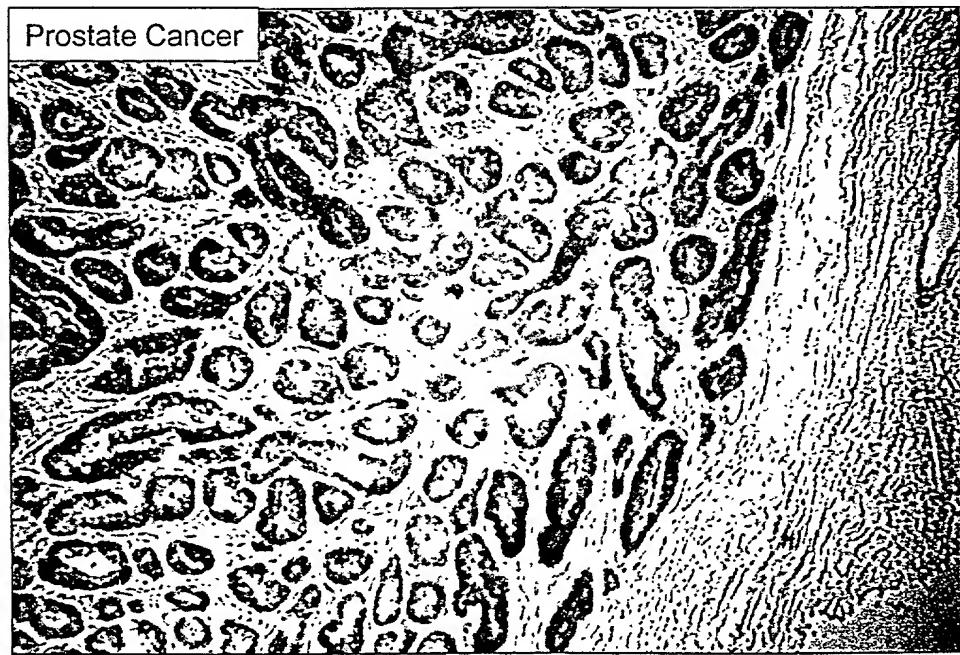


Figure 12A-12B

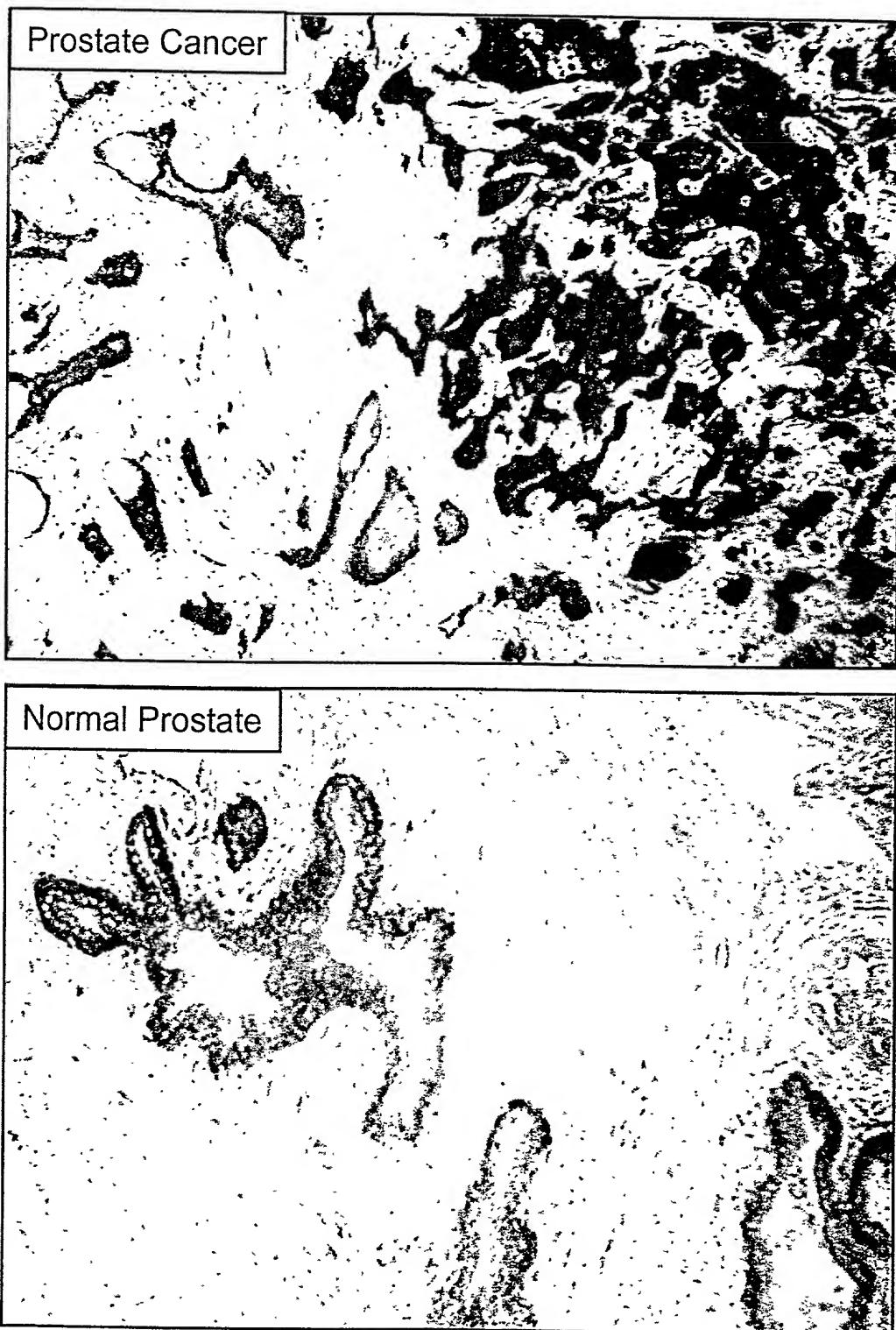


FIG. 13A

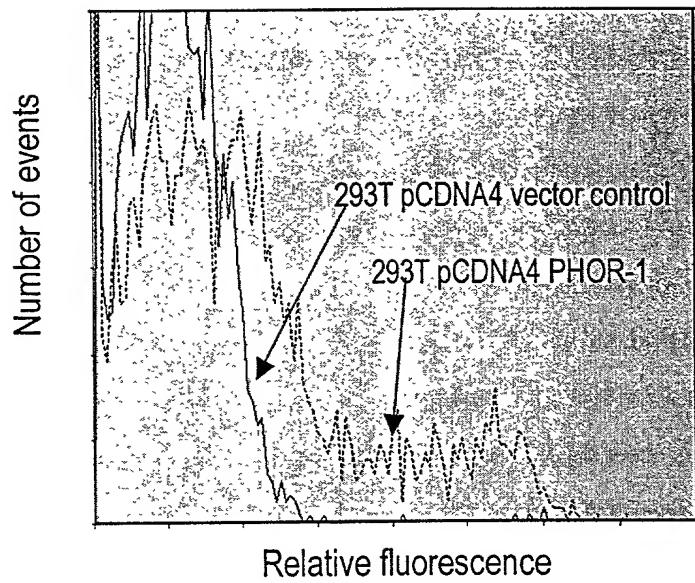


FIG. 13B

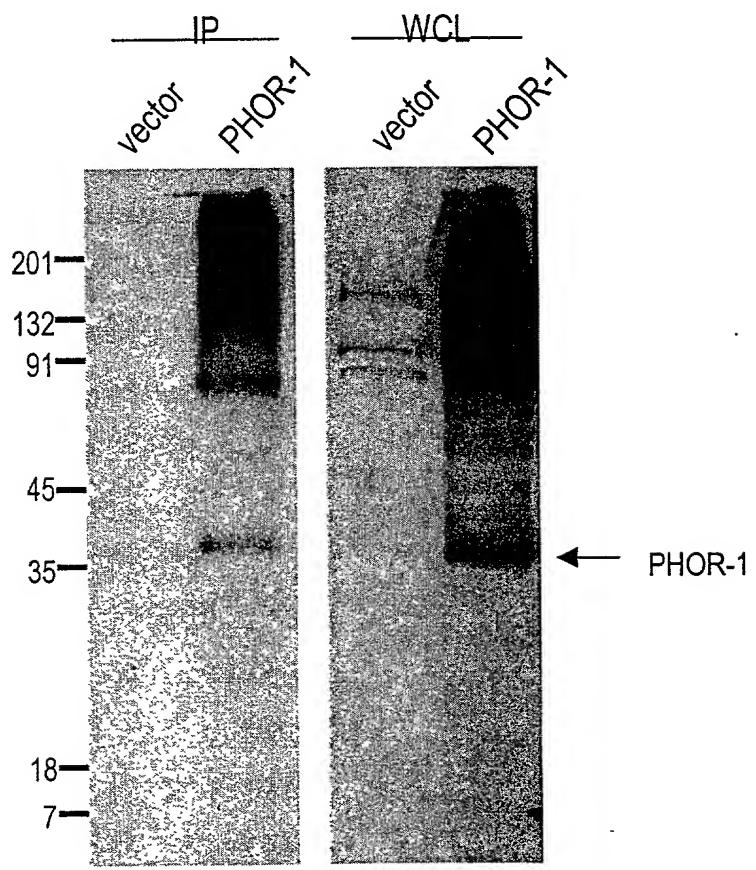


Fig. 14A

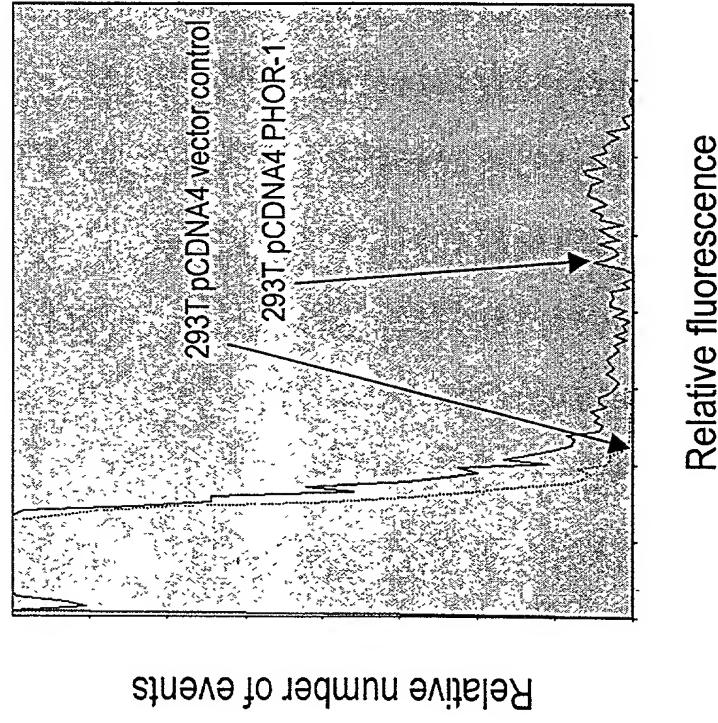


Fig. 14B

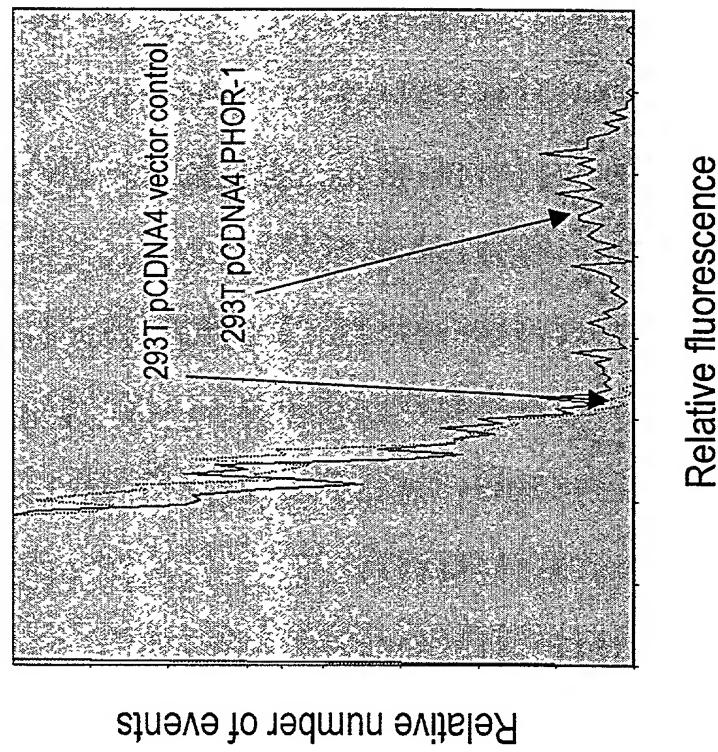


Fig. 15

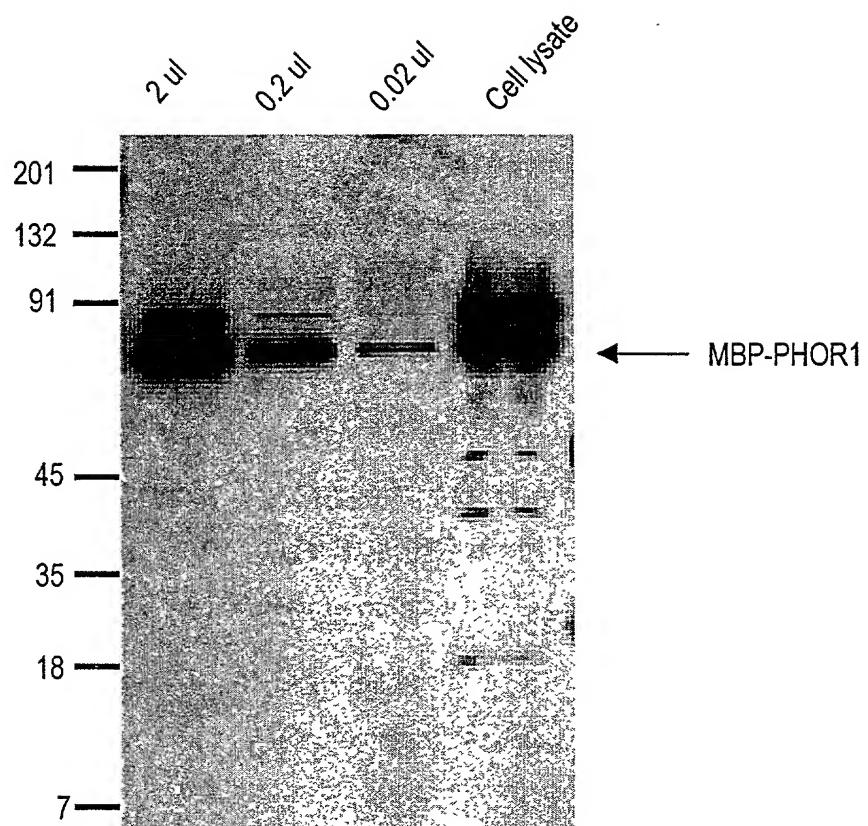


Fig. 16A

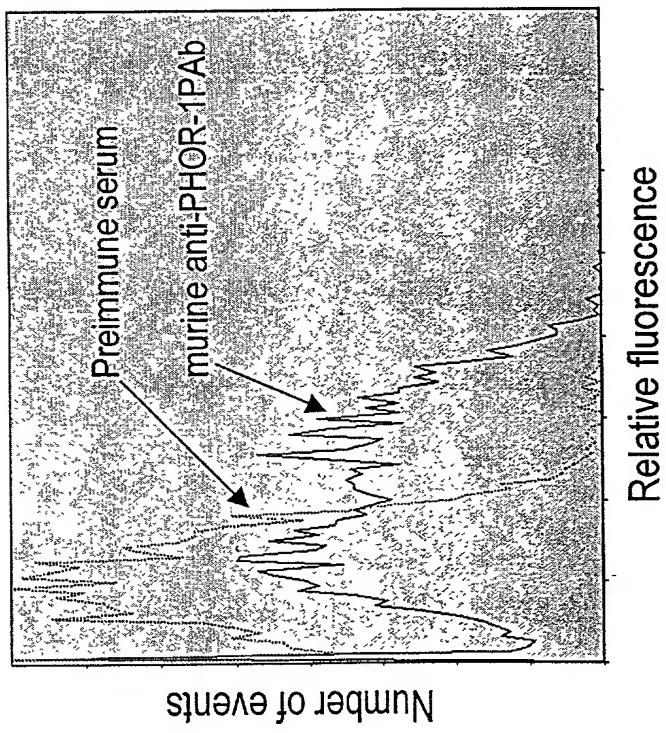
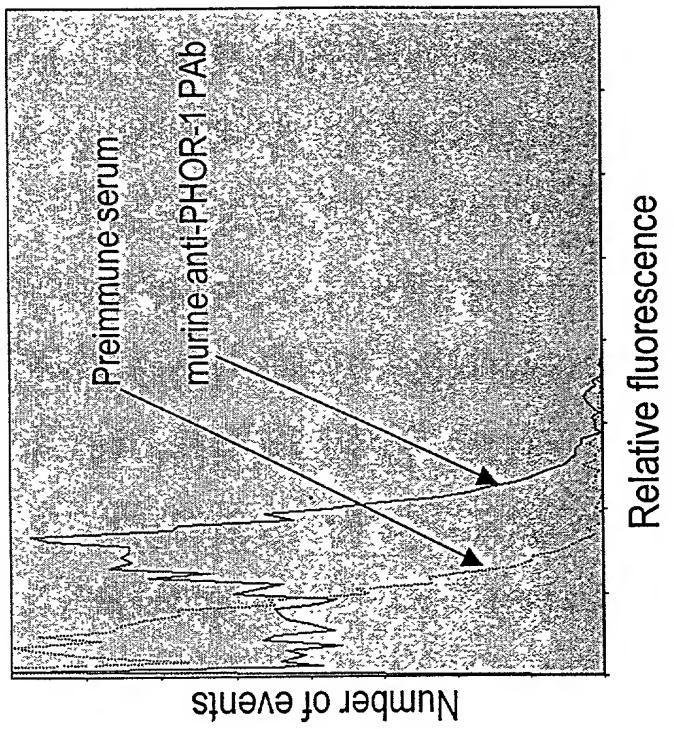


Fig. 16B



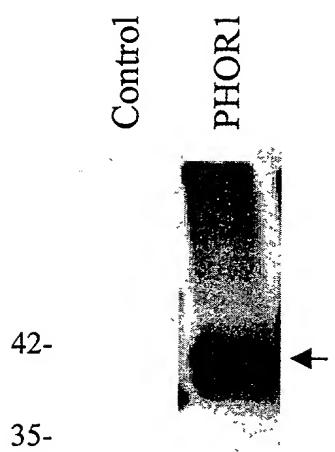


FIG. 17

Figure 18A-F

Fig. 18A. Prostate Cancer, 400X

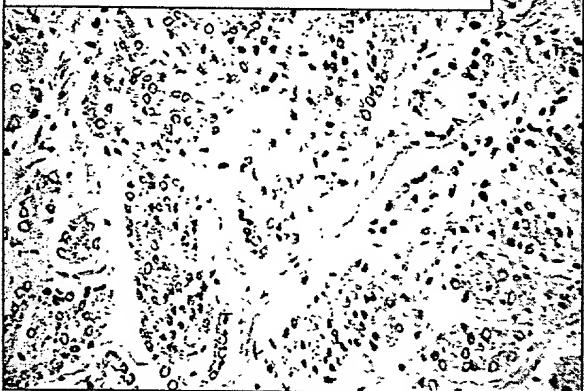


Fig. 18D. LNCaP, 400X

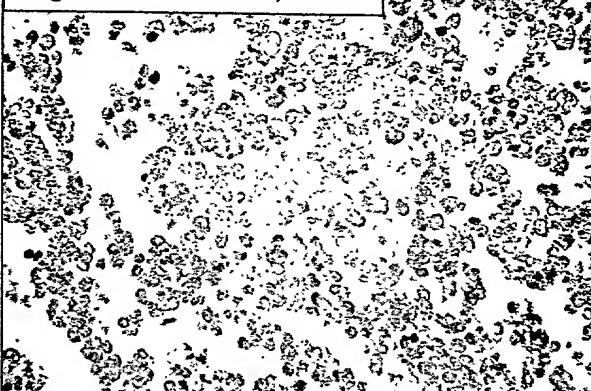


Fig. 18B. Prostate Cancer, 400X



Fig. 18E. Prostate, 400X



Fig. 18C. Prostate Cancer, 2000X

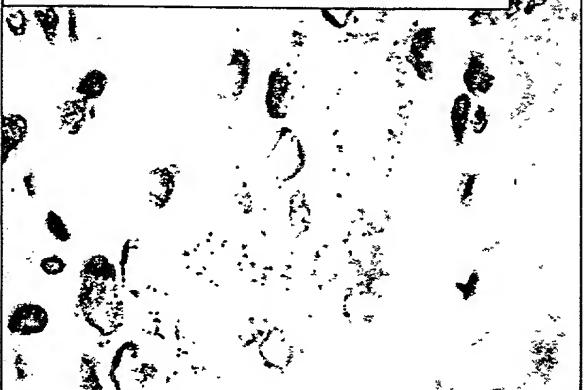


Fig. 18F. Prostate, 2000X



Figure 19A-F

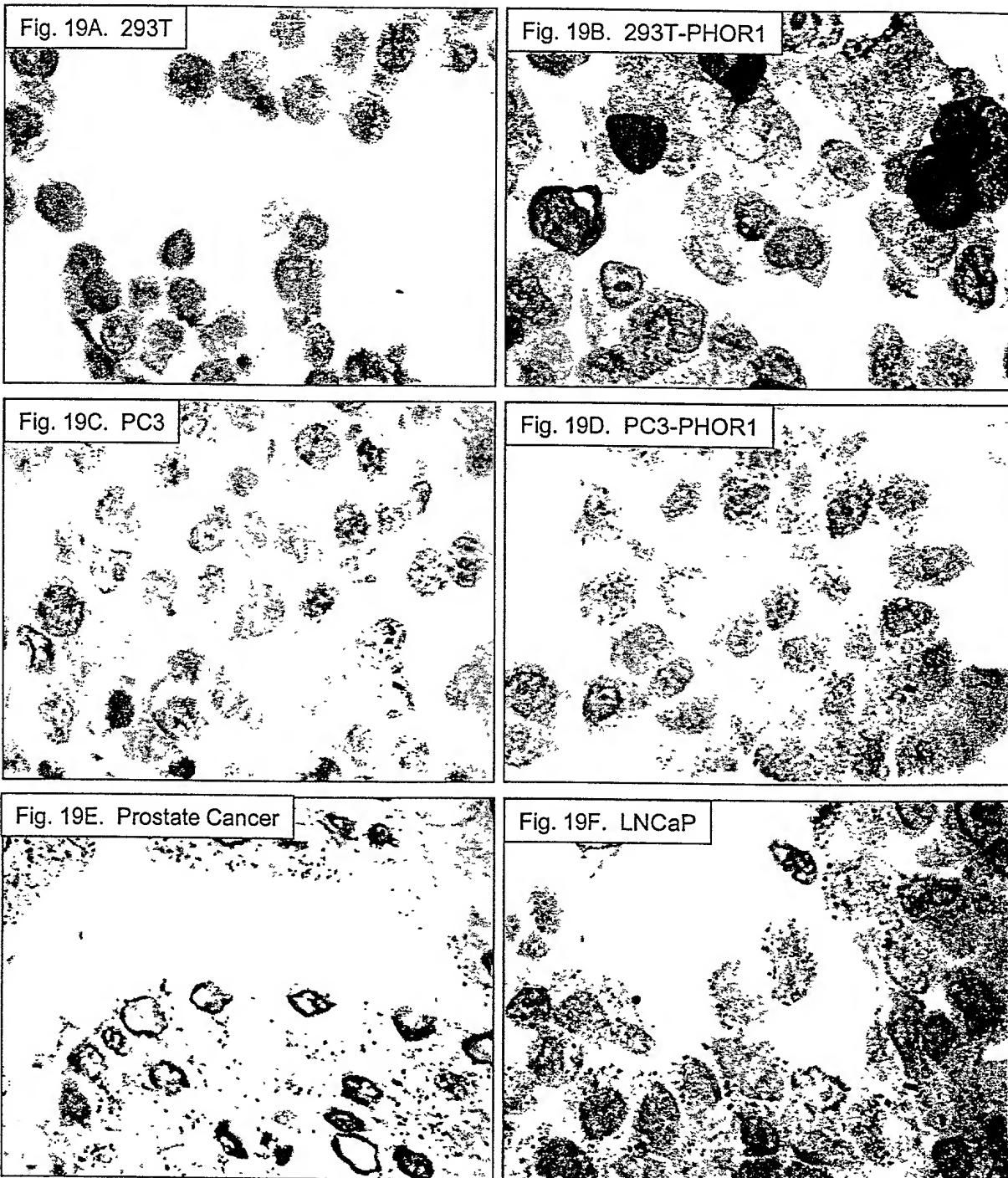


FIG. 20B

FIG. 20A

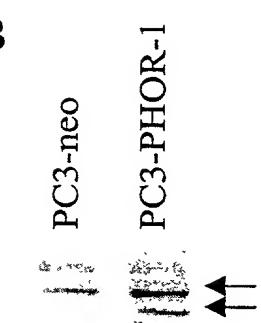
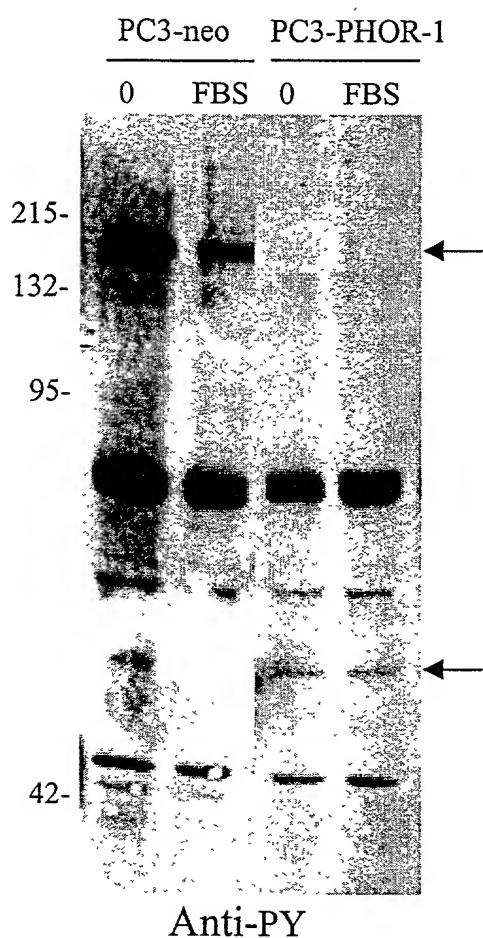


FIG. 20D

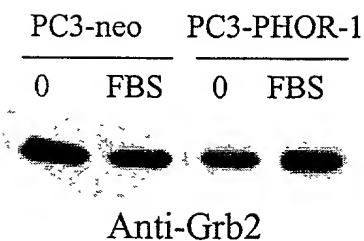
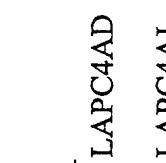
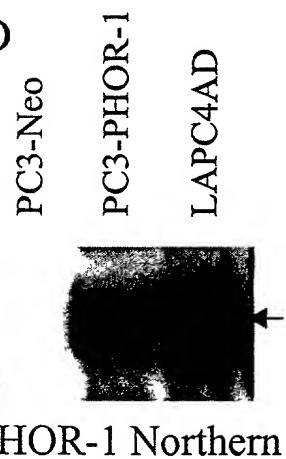


FIG. 20C

FIG. 20E

PHOR1 Northern

Neo



Fig. 21A

PHOR1



Fig. 21B

Ras

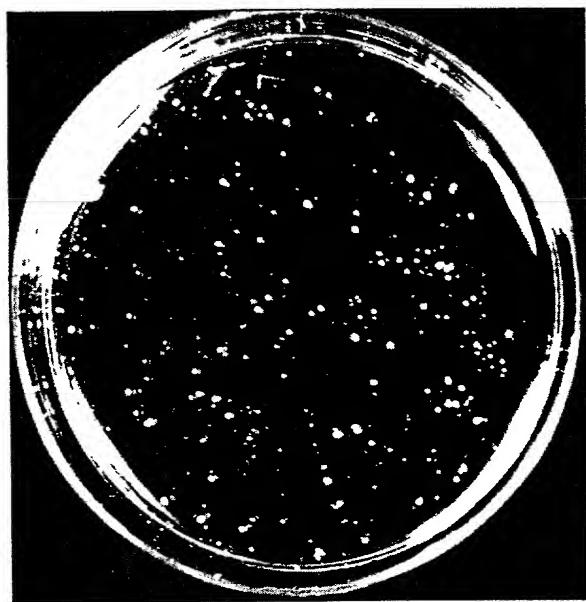


Fig. 21C

FIG. 22

	9	18	27	36	45	54
5'	GCT GTG GCC ATG TTT ATT GGA GTG TTG GAT CTA TTC TTT ATC ATC CTA TCT TAT					
	- - - - -	A V A M F I G V L D L F F I I I L S Y				
	63	72	81	90	99	108
	ATC TTT ATC CTT CAG GCA GTT CTA CAA CTC TCC TCT CAG GAG GCC CGC TAC AAA					
	- - - - -	I F I L Q A V L Q L S S Q E A R Y K				
	117	126	135	144	153	162
	GCA TTT GGG ACA TGT GTC TCT CAC ATA GGT GCC ATC TTA GCC TTC TAC ACA CCT					
	- - - - -	A F G T C V S H I G A I L A F Y T P				
	171	180	189	198	207	216
	TCA GTC ATC TCT TCA GTC ATG CAC CGT GTG GCC CGC TGT GCT GTG CCA CAC GTC					
	- - - - -	S V I S S V M H R V A R C A V P H V				
	225	234	243	252	261	270
	CAC ATT CTC CTC GCC AAT TTC TAT CTG CTC TTC CCA CCC ATG GTC AAT CCC ATC					
	- - - - -	H I L L A N F Y L L F P P M V N P I				
	279	288	297	306	315	324
	ATC TAT GGC GTT AAG ACC AAG CAG ATC CGT GAC AGT CTT GGG AGT ATT CCT GAG					
	- - - - -	I Y G V K T K Q I R D S L G S I P E				
	333	342	351	360	369	378
	AAA GGA TGT GTG AAT AGA GAG TGA GGA ATA AGT GGA AAA AGA GTG GGG CCC AGT					
	- - - - -	K G C V N R E *				
	387	396	405	414	423	432
	GAA TGC TGT AGT GGG CCA GGG CTG TGC TGA GAG TAG ATG GGT CCT AGA CTC CAC					
	- - - - -					
	441	450	459	468	477	486
	GTT TAG TTC TTT TCT TGT ATT ATG AAA AGA ATA AAT GAT GTC CTG AAG CTC AGA					
	- - - - -					
	495					
	AAA AAA AAA AAA AAA 3'					